
Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells.

Journal: Cell

Publication Year: 2013

Authors: Wei Xie, Matthew D Schultz, Ryan Lister, Zhonggang Hou, Nisha Rajagopal, Pradipta Ray, John W Whitaker, Shulan Tian, R David Hawkins, Danny Leung, Hongbo Yang, Tao Wang, Ah Young Lee, Scott A Swanson, Jiuchun Zhang, Yun Zhu, Audrey Kim, Joseph R Nery, Mark A Urich, Samantha Kuan, Chia-An Yen, Sarit Klugman, Pengzhi Yu, Kran Suknuntha, Nicholas E Propson, Huaming Chen, Lee E Edsall, Ulrich Wagner, Yan Li, Zhen Ye, Ashwinikumar Kulkarni, Zhenyu Xuan, Wen-Yu Chung, Neil C Chi, Jessica E Antosiewicz-Bourget, Igor Slukvin, Ron Stewart, Michael Q Zhang, Wei Wang, James A Thomson, Joseph R Ecker, Bing Ren

PubMed link: 23664764

Funding Grants: Mechanisms of chromatin dynamics at enhancers during ES cell differentiation

Public Summary:

Scientific Abstract:

Epigenetic mechanisms have been proposed to play crucial roles in mammalian development, but their precise functions are only partially understood. To investigate epigenetic regulation of embryonic development, we differentiated human embryonic stem cells into mesendoderm, neural progenitor cells, trophoblast-like cells, and mesenchymal stem cells and systematically characterized DNA methylation, chromatin modifications, and the transcriptome in each lineage. We found that promoters that are active in early developmental stages tend to be CG rich and mainly engage H3K27me3 upon silencing in nonexpressing lineages. By contrast, promoters for genes expressed preferentially at later stages are often CG poor and primarily employ DNA methylation upon repression. Interestingly, the early developmental regulatory genes are often located in large genomic domains that are generally devoid of DNA methylation in most lineages, which we termed DNA methylation valleys (DMVs). Our results suggest that distinct epigenetic mechanisms regulate early and late stages of ES cell differentiation.

Source URL: <https://www.cirm.ca.gov/about-cirm/publications/epigenomic-analysis-multilineage-differentiation-human-embryonic-stem-cells>